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A CONTRIBUTION TO THE GENETIC MAPPING OF RESISTANCE TO THE COTTON BLUE DISEASE USING SSR MARKERS

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One of the principal problems in the major cotton producing areas of Brazil is the occurrence of diseases, amongst which the Cotton Blue Disease has a major impact. The symptoms include a decrease in internode length, the reduction in plant, leaf and boll size, a clearing of the leaf veins that appear darker and curved downwards. The disease is caused by a Luteovirus, the Cotton Leafroll Dwarf Virus (CLDV) that is transmitted by aphids. The control of the disease relies on the control to a low level of the aphid vector, but most importantly on the availability to growers of resistant varieties. Resistance to the virus is inherited as a monogenic and dominant character. Screening germplasm for Blue Disease resistance under naatural conditions in the field is complicated by the fact that aphid infestation does not occur homogenously, which results in the possibility of escapes occurring. Thus, the identification of PCR-based molecular markers linked to Blue Disease resistance would be of great help to the cotton breeders in their efforts to breed disease resistant varieties.In order to identify such molecular markers linked to the resistance gene, an interspecific (*Gossypium hirsutum* var. DeltaOpal X *G. barbadense* MT121) F_2 mapping population was constructed. The parental genotypes were chosen such as the resistance stems from a cultivated cultivar while maximizing marker polymorphism through the use of a susceptible *G. barbadense* accession. Sixty-two individual plants of the F_2 population were used for DNA extraction and phenotyping for their response to virus inoculation, which was achieved under controlled conditions in the greenhouse by transferring infectious aphids to the plantlets. Microsatellite markers were chosen for their ability to produce clear amplification products and bands that are polymorphic between the two parental accessions. Results of the phenotyping confirm the simple inheritance - a single dominant gene - of the resistance in our population, thus validating the mapping population as a tool for marker identification. Genotyping results showed that a significant number of markers (17%) showed a distorted segregation; nevertheless, this level of distortion of segregation is similar to that observed in other similar cotton interspecific mapping populations. Put together, these results show that the present mapping population is adequate for the identification of molecular markers linked to Cotton Blue Disease resistance.

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